

SCORE Search Results Details for Application 10529592 and Search Result 20090427_122913_us-10-529-592a-1.rge.

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This page gives you Search Results detail for the Application 10529592 and Search Result 20090427_122913_us-10-529-592a-1.rge.

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OM nucleic - nucleic search, using sw model

Run on: April 28, 2009, 04:16:32 ; Search time 908 Seconds
(without alignments)
98090.438 Million cell updates/sec

Title: US-10-529-592A-1
Perfect score: 881
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14594359 seqs, 50548307366 residues

Total number of hits satisfying chosen parameters: 29188718

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
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 17: gb_htg3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	881	100.0	881	2	CQ800176	CQ800176 Sequence
	2	881	100.0	881	2	CS502806	CS502806 Sequence
	3	881	100.0	881	2	DD295744	DD295744 GENES AND
	4	827	93.9	893	2	CQ800178	CQ800178 Sequence
	5	827	93.9	893	2	CS502808	CS502808 Sequence
	6	827	93.9	893	2	DD295745	DD295745 GENES AND
c	7	611	69.4	614	2	DD131945	DD131945 Diagnosis
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c	12	547.4	62.1	160356	5	AC009068	AC009068 Homo sapi
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	14	433	49.1	447	2	CS539581	CS539581 Sequence
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	16	367	41.7	574	2	AX333084	AX333084 Sequence
	17	367	41.7	574	2	DL064480	DL064480 Cancer Ge
	18	261	29.6	229392	16	AC148906	AC148906 Otolemur
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	24	105.4	12.0	2721	2	AX593638	AX593638 Sequence
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	29	80.8	9.2	485	2	DL249991	DL249991 Organ-spe
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ALIGNMENTS

RESULT 1

CQ800176

LOCUS CQ800176 881 bp DNA linear PAT 28-APR-2004

DEFINITION Sequence 1 from Patent WO2004031411.

ACCESSION CQ800176

VERSION CQ800176.1 GI:46849094

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Nakamura,Y. and Katagiri,T.

TITLE Genes and polypeptides relating to human pancreatic cancers

JOURNAL Patent: WO 2004031411-A 1 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by The
President of the University of Tokyo (JP)

FEATURES Location/Qualifiers
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CDS 163..393
/note="unnamed protein product"
/codon_start=1
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ORIGIN

Query Match 100.0%; Score 881; DB 2; Length 881;

Best Local Similarity 100.0%; Pred. No. 7.1e-254;

Matches 881; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
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Qy	61	CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	61	CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
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Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCAGACATCATCATCACGCCCCCACCACACG	300
Db	241	GTCCTGAACGACAAGCACCTGGACGTGCCCAGACATCATCATCACGCCCCCACCACACG	300
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Db	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Db	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Qy	421	CTCCTGCTCCAGCGGCCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
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Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAACC CGGCCTCCGCTCAGAGAGACGTGGCAGG	540
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Qy 781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 840
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Qy 841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
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Db 841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881

RESULT 2
CS502806

LOCUS CS502806 881 bp DNA linear PAT 02-APR-2007

DEFINITION Sequence 1 from Patent WO2007013358.

ACCESSION CS502806

VERSION CS502806.1 GI:138982984

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Nakamura,Y., Katagiri,T. and Inaki,K.

TITLE Vivit polypeptides, therapeutic agent comprising the same, and
method of screening for anti-cancer agent

JOURNAL Patent: WO 2007013358-A 1 01-FEB-2007;
The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)

FEATURES Location/Qualifiers

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CDS 163. .393
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ORIGIN

Query Match 100.0%; Score 881; DB 2; Length 881;
Best Local Similarity 100.0%; Pred. No. 7.1e-254;
Matches 881; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGCCCCCGAGCCCGAC 60

Db	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Qy	61	CGCCGCCGCCACCACCACCAGCGCCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	61	CGCCGCCGCCACCACCACCAGCGCCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCACG	300
Db	241	GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCACG	300
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Db	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Db	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Db	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAACC CGGCCTCCGCTCAGAGAGACGTGGCAGG	540
Db	481	CTGAATACCCTGGATGGGAACTGAGCGAACC CGGCCTCCGCTCAGAGAGACGTGGCAGG	540
Qy	541	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGAGTG	600
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Qy	601	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA	660
Db	601	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA	660
Qy	661	TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	720
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Qy	721	CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	780
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Qy 781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 840
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Db 841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881

RESULT 3
DD295744

LOCUS DD295744 881 bp DNA linear PAT 16-AUG-2006
DEFINITION GENES AND POLYPEPTIDES RELATING TO HUMAN PANCREATIC CANCERS.
ACCESSION DD295744
VERSION DD295744.1 GI:112721854
KEYWORDS JP 2006500947-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 881)
AUTHORS Nakamura,Y. and Katagiri,T.
TITLE GENES AND POLYPEPTIDES RELATING TO HUMAN PANCREATIC CANCERS
JOURNAL Patent: JP 2006500947-A 1 12-JAN-2006;
ONCOTHERAPY SCIENCE INC, JAPAN AS REPRESENTED BY THE PRESIDENT OF
THE UNIVERSITY OF TOKYO

COMMENT OS Homo sapiens
PN JP 2006500947-A/1
PD 12-JAN-2006
PF 12-SEP-2003 JP 2004541224
PR 30-SEP-2002 US 60/414872,28-FEB-2003 US 60/450889 PI
yusuke nakamura,toyomasa katagiri
CC
FH Key Location/Qualifiers
FT CDS (163)..(390).

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 881; DB 2; Length 881;
Best Local Similarity 100.0%; Pred. No. 7.1e-254;
Matches 881; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGCCCCCGAGCCCGAC 60
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Db 1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGCCCCCGAGCCCGAC 60

Qy	61	CGCCGCCGCCACCACCACCAGCGCCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	61	CGCCGCCGCCACCACCACCAGCGCCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCAGACATCATCATCACGCCCCCACCACG	300
Db	241	GTCCTGAACGACAAGCACCTGGACGTGCCCAGACATCATCATCACGCCCCCACCACG	300
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Db	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Db	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Db	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAACC CGGCCTCCGCTCAGAGAGACGTGGCAGG	540
Db	481	CTGAATACCCTGGATGGGAACTGAGCGAACC CGGCCTCCGCTCAGAGAGACGTGGCAGG	540
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Db	601	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA	660
Qy	661	TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	720
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Qy	721	CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	780
Db	721	CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	780
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Db 781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 840

Qy 841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
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Db 841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881

RESULT 4
CQ800178

LOCUS CQ800178 893 bp DNA linear PAT 28-APR-2004

DEFINITION Sequence 3 from Patent WO2004031411.

ACCESSION CQ800178

VERSION CQ800178.1 GI:46849096

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Nakamura,Y. and Katagiri,T.

TITLE Genes and polypeptides relating to human pancreatic cancers

JOURNAL Patent: WO 2004031411-A 3 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by The
President of the University of Tokyo (JP)

FEATURES Location/Qualifiers

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/db_xref="GI:46849097"
/translation="MGLKMSCLKAAAAATTRPPS"

ORIGIN

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Best Local Similarity 97.5%; Pred. No. 1.4e-237;
Matches 859; Conservative 0; Mismatches 0; Indels 22; Gaps 1;

Qy 1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGCCCCCGAGCCCGAC 60
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Db 35 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGCCCCCGAGCCCGAC 94

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Db 95 CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC 154

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Db	253	GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACG	312
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Db	313	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	372
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Db	373	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	432
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Db	613	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA	672
Qy	661	TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	720
Db	673	TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	732
Qy	721	CCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	780
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Db	853	ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	893

RESULT 5
CS502808
LOCUS CS502808 893 bp DNA linear PAT 02-APR-2007
DEFINITION Sequence 3 from Patent WO2007013358.
ACCESSION CS502808
VERSION CS502808.1 GI:138982991
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Nakamura,Y., Katagiri,T. and Inaki,K.
TITLE Vivit polypeptides, therapeutic agent comprising the same, and
method of screening for anti-cancer agent
JOURNAL Patent: WO 2007013358-A 3 01-FEB-2007;
The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)

FEATURES Location/Qualifiers
source 1. .893
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
CDS 197. .259
/note="unnamed protein product"
/codon_start=1
/protein_id="CAM83961.1"
/db_xref="GI:138982992"
/translation="MGLKMSCLKAAAAATTRPPS"

ORIGIN

Query Match 93.9%; Score 827; DB 2; Length 893;
Best Local Similarity 97.5%; Pred. No. 1.4e-237;
Matches 859; Conservative 0; Mismatches 0; Indels 22; Gaps 1;

Qy	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Db	35	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	94
Qy	61	CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	95	CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	154
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	155	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	214
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240

http://es/ScoreAccessWeb/GetItem.action?AppId=105295...7_122913_us-10-529-592a-1.rge&ItemType=4&startByte=0 (12 of 35)5/19/2009 9:51:03 AM

DEFINITION GENES AND POLYPEPTIDES RELATING TO HUMAN PANCREATIC CANCERS.
ACCESSION DD295745
VERSION DD295745.1 GI:112721855
KEYWORDS JP 2006500947-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS Nakamura,Y. and Katagiri,T.
TITLE GENES AND POLYPEPTIDES RELATING TO HUMAN PANCREATIC CANCERS
JOURNAL Patent: JP 2006500947-A 2 12-JAN-2006;
ONCOTHERAPY SCIENCE INC, JAPAN AS REPRESENTED BY THE PRESIDENT OF
THE UNIVERSITY OF TOKYO
COMMENT OS Homo sapiens
PN JP 2006500947-A/2
PD 12-JAN-2006
PF 12-SEP-2003 JP 2004541224
PR 30-SEP-2002 US 60/414872,28-FEB-2003 US 60/450889 PI
yusuke nakamura,toyomasa katagiri
CC
FH Key Location/Qualifiers
FT CDS (197)..(256).
FEATURES Location/Qualifiers
source 1..893
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 93.9%; Score 827; DB 2; Length 893;
Best Local Similarity 97.5%; Pred. No. 1.4e-237;
Matches 859; Conservative 0; Mismatches 0; Indels 22; Gaps 1;

Qy	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Db	35	GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	94
Qy	61	CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	95	CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	154
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	155	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	214
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	215	TGCCTGAA-----AGCAGCAGCAGCAGCCACGACGAGGCCCCC	252

Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCC	GACATCATCATCACGCCCCC	ACCCCCACG	300
Db	253	GTCCTGAACGACAAGCACCTGGACGTGCCC	GACATCATCATCACGCCCCC	ACCCCCACG	312
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGG	GAGCACAGTCTGGCTGGATGAGACAGGGT	CGTGC	360
Db	313	GGCATGATGCTGCCGAGGGACTTGGGG	GAGCACAGTCTGGCTGGATGAGACAGGGT	CGTGC	372
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG			420
Db	373	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG			432
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG			480
Db	433	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG			492
Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG			540
Db	493	CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG			552
Qy	541	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGAGTG			600
Db	553	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCGCTGAGTG			612
Qy	601	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA			660
Db	613	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA			672
Qy	661	TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG			720
Db	673	TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG			732
Qy	721	CCCCCAGGGCTGTGCAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG			780
Db	733	CCCCCAGGGCTGTGCAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG			792
Qy	781	TGGAGTGGCTGTTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT			840
Db	793	TGGAGTGGCTGTTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT			852
Qy	841	ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC			881
Db	853	ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC			893

RESULT 7
DD131945/c
LOCUS DD131945 614 bp DNA linear PAT 04-NOV-2005
DEFINITION Diagnosis and Prognosis of Breast Cancer Patients.
ACCESSION DD131945

VERSION DD131945.1 GI:92825448

KEYWORDS JP 2005500832-A/2531.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 614)

AUTHORS Bernard, R., Vijver, M.J.V.D., Veer, L.J.V., Roberts, C.J., Mao, M., Linsley, P.S., He, Y., Dai, H. and Hart, A.A.M.

TITLE Diagnosis and Prognosis of Breast Cancer Patients

JOURNAL Patent: JP 2005500832-A 2531 13-JAN-2005; Rosetta Inpharmatics

COMMENT OS Homo sapiens

PN JP 2005500832-A/2531

PD 13-JAN-2005

PF 14-JUN-2002 JP 2003505588

PR 18-JUN-2001 US 60/298918, 14-MAY-2002 US 60/380710 PI rene bernards, marc j van de vijver, laura johanna van't veer, PI christopher j roberts, mao mao, peter s linsley, yudong he, PI hongyue dai,

PI a a m hart

CC

FH Key Location/Qualifiers.

FEATURES Location/Qualifiers

source 1..614

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 69.4%; Score 611; DB 2; Length 614;

Best Local Similarity 100.0%; Pred. No. 2.2e-172;

Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GACATCATCATCACGCCCCCACCACCGGGCATGATGCTGCCGAGGGACTTGGGGAGC 330

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Db 614 GACATCATCATCACGCCCCCACCACCGGGCATGATGCTGCCGAGGGACTTGGGGAGC 555

Qy 331 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC 390

|||||

Db 554 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC 495

Qy 391 TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT 450

|||||

Db 494 TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT 435

Qy 451 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAAC 510

|||||

Db 434 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAAC 375

Qy	511	CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC	570
Db	374	CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC	315
Qy	571	AGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG	630
Db	314	AGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG	255
Qy	631	CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAG	690
Db	254	CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAG	195
Qy	691	GCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTG	750
Db	194	GCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTG	135
Qy	751	CCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTA	810
Db	134	CCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTA	75
Qy	811	CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGA	870
Db	74	CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGA	15
Qy	871	TCCTCTGTAAC	881
Db	14	TCCTCTGTAAC	4

RESULT 8
DD417196/c
LOCUS DD417196 614 bp DNA linear PAT 26-MAR-2007
DEFINITION Diagnosis and Prognosis of Breast Cancer Patients.
ACCESSION DD417196
VERSION DD417196.1 GI:134130622
KEYWORDS JP 2006519591-A/2531.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 614)
AUTHORS He,Y. and Veer,L.J.V.
TITLE Diagnosis and Prognosis of Breast Cancer Patients
JOURNAL Patent: JP 2006519591-A 2531 31-AUG-2006;
Rosetta Inpharmatics LLC JUERGEN HERMANN NETT
COMMENT OS Homo sapiens
PN JP 2006519591-A/2531
PD 31-AUG-2006
PF 15-JAN-2004 JP 2006500977

PR 15-JAN-2003 US 10/342887
PI yudong he,laura johanna van't veer
CC
FH Key Location/Qualifiers.

FEATURES Location/Qualifiers
source 1. .614
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 69.4%; Score 611; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;
Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	271	GACATCATCATCACGCCCCCACCACCGGGCATGATGCTGCCGAGGGACTTGGGGAGC	330
Db	614	GACATCATCATCACGCCCCCACCACCGGGCATGATGCTGCCGAGGGACTTGGGGAGC	555
Qy	331	ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC	390
Db	554	ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC	495
Qy	391	TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT	450
Db	494	TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT	435
Qy	451	CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAAC	510
Db	434	CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAAC	375
Qy	511	CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC	570
Db	374	CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC	315
Qy	571	AGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG	630
Db	314	AGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG	255
Qy	631	CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAG	690
Db	254	CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAG	195
Qy	691	GCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTG	750
Db	194	GCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTG	135
Qy	751	CCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTA	810
Db	134	CCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTA	75

Qy 811 CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGA 870
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Db 74 CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGA 15

Qy 871 TCCTCTGTAAC 881
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Db 14 TCCTCTGTAAC 4

RESULT 9

EA064706/c

LOCUS EA064706 614 bp DNA linear PAT 07-FEB-2007

DEFINITION Sequence 2531 from patent US 7171311.

ACCESSION EA064706

VERSION EA064706.1 GI:125176216

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 614)

AUTHORS Dai,H., He,Y., Linsley,P.S., Mao,M., Roberts,C.J., Van't Veer,L.J.,
Van de Vijver,M.J., Bernards,R. and Hart,A.A.M.

TITLE Methods of assigning treatment to breast cancer patients

JOURNAL Patent: US 7171311-A 2531 30-JAN-2007;
Rosetta Inpharmatics LLC and Netherlands Cancer Institute; Seattle,
WA;
US;

FEATURES Location/Qualifiers

source 1..614
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 69.4%; Score 611; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;
Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GACATCATCATCACGCCCCCACCACGGGCATGATGCTGCCGAGGGACTTGGGGAGC 330
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Db 614 GACATCATCATCACGCCCCCACCACGGGCATGATGCTGCCGAGGGACTTGGGGAGC 555

Qy 331 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC 390
|||||

Db 554 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC 495

Qy 391 TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT 450
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Db 494 TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT 435

Qy 451 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAAC 510

Db	434		CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAAC	375
Qy	511		CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC	570
Db	374		CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC	315
Qy	571		AGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG	630
Db	314		AGAACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG	255
Qy	631		CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAG	690
Db	254		CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAG	195
Qy	691		GCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCTG	750
Db	194		GCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCTG	135
Qy	751		CCATAAGCACCAACAAGAAGTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTA	810
Db	134		CCATAAGCACCAACAAGAAGTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTA	75
Qy	811		CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGA	870
Db	74		CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGA	15
Qy	871		TCCTCTGTAAC	881
Db	14		TCCTCTGTAAC	4

RESULT 10
AC123908/c

LOCUS	AC123908	185321 bp	DNA	linear	PRI 28-MAR-2003
DEFINITION	Homo sapiens chromosome 16 clone CTD-2542L18, complete sequence.				
ACCESSION	AC123908				
VERSION	AC123908.3 GI:29336199				
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 185321)				
AUTHORS	DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.				
TITLE	Direct Submission				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 185321)				

AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 185321)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 185321)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 28, 2003 this sequence version replaced gi:22748376.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
FEATURES Location/Qualifiers
source 1. .185321
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="CTD-2542L18"

ORIGIN

Query Match 62.3%; Score 549; DB 5; Length 185321;
Best Local Similarity 100.0%; Pred. No. 1.2e-153;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 333 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 392
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Db 124973 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 124914

Qy 393 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
|||||
Db 124913 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 124854

Qy 453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 512
|||||
Db 124853 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 124794

Qy 513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
|||||
Db 124793 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 124734

Qy	573	AACAGTGT	TTCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	632
Db	124733	AACAGTGT	TTCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	124674
Qy	633	GACTCCGGCCTGGT	GAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC	692
Db	124673	GACTCCGGCCTGGT	GAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC	124614
Qy	693	TCTCTTCTGGACA	AAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCC	752
Db	124613	TCTCTTCTGGACA	AAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCC	124554
Qy	753	ATAAGCACCAACA	AAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA	812
Db	124553	ATAAGCACCAACA	AAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA	124494
Qy	813	GATACGGAAACAGT	CCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC	872
Db	124493	GATACGGAAACAGT	CCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC	124434
Qy	873	CTCTGTAAC	881	
Db	124433	CTCTGTAAC	124425	

RESULT 11				
AC018695/c				
LOCUS	AC018695	211001 bp	DNA	linear PRI 09-JAN-2002
DEFINITION	Homo sapiens BAC clone RP11-568J23 from 16, complete sequence.			
ACCESSION	AC018695			
VERSION	AC018695.6 GI:13443271			
KEYWORDS	HTG.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 211001)			
AUTHORS	Sulston,J.E. and Waterston,R.			
TITLE	Toward a complete human genome sequence			
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)			
PUBMED	9847074			
REFERENCE	2 (bases 1 to 211001)			
AUTHORS	Haakenson,W., Scott,K., Courtney,L., Drone,K., Gregory,S. and Lesley,K.			
TITLE	The sequence of Homo sapiens BAC clone RP11-568J23			
JOURNAL	Unpublished (2001)			
REFERENCE	3 (bases 1 to 211001)			
AUTHORS	Waterston,R.H.			

TITLE Direct Submission
JOURNAL Submitted (16-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 211001)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 211001)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 6 (bases 1 to 211001)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Mar 24, 2001 this sequence version replaced gi:9838280.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0568J23
-----.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male

donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-542M13. Actual start of this clone is at base position 1 of RP11-568J23; actual end is at base position 211001 of RP11-568J23.

H_NH0568J23 contains an imperfect GA run from 143896 to 144293, in which the exact length is unknown. There are approximately 800 bases missing according to the restriction digests and pcr data.

H_NH0568J23 contains a single stranded region from 144079 to 144172 which contains low quality data.

FEATURES	Location/Qualifiers
source	1. .211001 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="16" /map="16" /clone="RP11-568J23" /clone_lib="RPCI-11"
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repeat_region	407. .467 /rpt_family="MIR"
repeat_region	760. .835 /rpt_family="MIR"
repeat_region	891. .929 /rpt_family="MER1_type"
repeat_region	939. .1114 /rpt_family="L1"
repeat_region	1115. .1254 /rpt_family="Alu"
repeat_region	1255. .1555 /rpt_family="Alu"
repeat_region	1530. .1555 /rpt_family="(A)n"
repeat_region	1556. .1723 /rpt_family="Alu"
repeat_region	1724. .2020 /rpt_family="L1"
repeat_region	2023. .2332 /rpt_family="Alu"

repeat_region	2334. .2455
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repeat_region	2672. .2776
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repeat_region	2793. .3021
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repeat_region	3022. .3340
	/rpt_family="Alu"
repeat_region	3024. .3051
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	/note="match to EST AA760709 (NID:g2809639) nz13c11.s1"
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repeat_region	3914. .4009
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repeat_region	4291. .4349
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repeat_region	4367. .4677
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repeat_region	5175. .5260
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repeat_region	5722. .5819
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	/rpt_family="L2"
repeat_region	6092. .6370
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repeat_region	8334. .8424
	/rpt_family="MIR"
repeat_region	8499. .8616


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misc_feature      9455. .10166
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repeat_region     9817. .9909
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repeat_region     9939. .10037
                  /rpt_family="MIR"
repeat_region     10041. .10172
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repeat_region     10590. .10611
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Query Match 62.3%; Score 549; DB 5; Length 211001;
 Best Local Similarity 100.0%; Pred. No. 1.2e-153;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      333 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 392
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Db      17960 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 17901

Qy      393 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
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Db      17900 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 17841

Qy      453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 512
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Db      17840 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 17781

Qy      513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
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Qy      573 AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 632
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Db      17720 AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 17661

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Qy	633	GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC	692
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Qy	693	TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCCTGCC	752
Db	17600	TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCCTGCC	17541
Qy	753	ATAAGCACCAACAAGAAGCTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA	812
Db	17540	ATAAGCACCAACAAGAAGCTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA	17481
Qy	813	GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC	872
Db	17480	GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC	17421
Qy	873	CTCTGTAAC	881
Db	17420	CTCTGTAAC	17412

RESULT 12

AC009068/c

LOCUS AC009068 160356 bp DNA linear PRI 27-APR-2001

DEFINITION Homo sapiens chromosome 16 clone RP11-314K3, complete sequence.

ACCESSION AC009068

VERSION AC009068.10 GI:13811892

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 160356)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 160356)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 160356)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (27-APR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Apr 27, 2001 this sequence version replaced gi:12000278.

FEATURES Location/Qualifiers

source 1. .160356

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/note="Draft Sequence Produced by DOE Joint Genome
Institute;
www.jgi.doe.gov;
Finishing Completed at Stanford Human Genome Center;
www-shgc.stanford.edu;
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.3.;
STS Content;;
WI-11796 G24048;
SHGC-37143 G30481"

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ORIGIN

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Query Match          62.1%;  Score 547.4;  DB 5;  Length 160356;
Best Local Similarity 99.8%;  Pred. No. 3.6e-153;
Matches 548;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      333 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 392
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Db      79810 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 79751

Qy      393 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
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Db      79750 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 79691

Qy      453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGGAGCGAAGCC 512
          |||
Db      79690 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGGAGCGAAGCC 79631

Qy      513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
          |||
Db      79630 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 79571

Qy      573 AACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 632
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Db      79570 AACAGTGTTTCCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 79511

Qy      633 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC 692
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Qy      693 TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCCTGCC 752
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Qy 753 ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 812
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Qy 813 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 872
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Db 79330 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 79271

Qy 873 CTCTGTAAC 881
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Db 79270 CTCTGTAAC 79262

RESULT 13
AC202720/c

LOCUS AC202720 189224 bp DNA linear HTG 29-MAY-2008
DEFINITION Pan troglodytes chromosome 16 clone CH251-467D6, WORKING DRAFT
SEQUENCE.
ACCESSION AC202720
VERSION AC202720.2 GI:189163682
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 189224)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2007) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 2 (bases 1 to 189224)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2008) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On May 29, 2008 this sequence version replaced gi:145587712.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: C_AB0467D06

----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319
Consensus quality: 188692 bases at least Q40
Consensus quality: 188913 bases at least Q30
Consensus quality: 189064 bases at least Q20

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 189224: contig of 189224 bp in length.

FEATURES
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/organism="Pan troglodytes"
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clone_end:SP6;
vector_side:right"

ORIGIN		Query Match 61.6%; Score 542.6; DB 16; Length 189224;	
		Best Local Similarity 99.3%; Pred. No. 1e-151;	
		Matches 545; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Qy	333	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	392
Db	116593	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	116534
Qy	393	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	452
Db	116533	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	116474
Qy	453	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC	512
Db	116473	GGGGGTGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAATCC	116414
Qy	513	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG	572
Db	116413	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCAAGGAATCCAGCCTGCCCACTTCCAG	116354
Qy	573	AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	632
Db	116353	AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	116294

Qy 633 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC 692
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Db 116293 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC 116234

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Qy 813 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 872
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Qy 873 CTCTGTAAC 881
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Db 116053 CTCTGTAAC 116045

RESULT 14
CS539581

LOCUS CS539581 447 bp DNA linear PAT 20-APR-2007

DEFINITION Sequence 168 from Patent WO2007012811.

ACCESSION CS539581

VERSION CS539581.1 GI:145584734

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Maitland,N. and Bryce,S.

TITLE Stem cell markers

JOURNAL Patent: WO 2007012811-A 168 01-FEB-2007;
Procure Therapeutics Limited (GB)

FEATURES Location/Qualifiers

source 1. .447
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 49.1%; Score 433; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.2e-118;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGCCCCCGAGCCCGAC 60

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Db	75	 CGCCGCCGCCACCACCACCAGCGCCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	134
Qy	121	AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	135	 AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	194
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	195	 TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	254
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCAGACATCATCATCACGCCCCCACCACCCACG	300
Db	255	 GTCCTGAACGACAAGCACCTGGACGTGCCCAGACATCATCATCACGCCCCCACCACCCACG	314
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
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Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Db	375	 CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	434
Qy	421	CTCCTGCTCCAGC	433
Db	435	 CTCCTGCTCCAGC	447

RESULT 15
AC198304/c

LOCUS	AC198304	195676 bp	DNA	linear	HTG 14-APR-2007
DEFINITION	Macaca mulatta clone CH250-65C9, WORKING DRAFT SEQUENCE, 4 ordered pieces.				
ACCESSION	AC198304				
VERSION	AC198304.4 GI:145279267				
KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLLTOP.				
SOURCE	Macaca mulatta (rhesus monkey)				
ORGANISM	Macaca mulatta Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.				
REFERENCE	1 (bases 1 to 195676)				
AUTHORS	Muzny,D.M., Abraham,K.K., Abulimiti,A., Adams,C.Q., Aduba,G., Allen,C.C., Alsbrooks,S.L., Anosike,U.S., Archer,P.M., Arredondo,H.H., Attaway,T., Bandaranaike,D.P., Bangura,L., Barton,S.R., Bell,A.V., Bell,S.N., Beraducci,A.R., Bickham,C.,				

Biswalo,K., Blyth,P.R., Buhay,C.J., Canada,A., Cardenas,V.,
 Carter,K., Chacko,J., Chandrabose,M.N., Chavez,A., Chavez,D.,
 Chen,G., Chen,R., Chu,H., Clerc blankenburg,K.P., Cockrell,R.,
 Cooper,J.A., Coyle,M.D., Cree,A., Cueto,C.B., Curry,S.M., Dai,W.,
 Dao,M.D., Davila,M., Davis,C., Davy-Carroll,L., Del fierro,P.,
 Demen,R., Denson,S., Ding,Y., Dinh,H.H., Donlin,J.E.,
 Dugan-Rocha,S., Dunn,A.M., Durbin,K.J., Ebong,V.E., Egan,A.,
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 Flagg,N., Forbes,L.D., Fowler,R.G., Fu,Q., Fuh,E., Gabisi,R.A.,
 Ganardhanan,M., Ganer,J., Garcia iii,R.M., Garcia,A.M.,
 Garcia,S.M., Garner,T.T., Ghose,S., Gingras,M.,
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 Hagans,B.J., Hall,O., Hamid,H., Hamilton,K.A., Hampton,O.A.,
 Harbes,B.A., Harris,R.A., Havlak,P., Hawes,A.C., Hawkins,E.S.,
 Haynes,S.J., Hemphill,L., Hernandez,J., Hines,S., Hirani,K.,
 Hitchens,M.E., Hodgson,A.V., Hagues,M.E., Holder,M., Hollins,B.,
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 Joshi,V., Joy,C., Kaikai,F.B., Kalafus,K.J., Kalu,J.B., Kang,Y.,
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 Kowis,A.N., Kowis,C.R., Lago,L.A., Lago,M.T., Lai,C., Lara,F.,
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 Lewis,L.R., Li,B., Li,Y., Li,Z., Linnell,M.A., Liu,J., Liu,W.,
 Liu,Y., Liu,Y., Liyanage,D., London,P., Lopez,J., Lorensuhewa,L.M.,
 Lozado,R.J., Luc,T., Madu,R.C., Maheshwari,M., Maheshwari,R.,
 Malloy,K., Mansouri,D.L., Martinez,E., Matejkova,P., Mathew,T.,
 Mccauley,S.K., Mcpherson,J.D., Mercado,C., Mercado,I.C.,
 Metzker,M.L., Millin,A., Milosavljevic,A., Morgan,M.B., Morris,S.,
 Munidasa,M., Murray,D.D., Muzny,D.M., Nazareth,L.V., Ngo,D.N.,
 Nguyen,H.T., Nguyen,N.B., Nguyen,P.Q., Nwaokelemeh,O.O.,
 Obregon,M., Odeh,E.A., Okonkwo,F., Okwuonu,G.O., Okwuonu,K.C.,
 Onyenekwe,J., Parish,B.J., Parker,D.N., Parra,A.A., Pasternak,S.,
 Patel,B.M., Patel,R.R., Paul,H.A., Perez,A., Perez,L.M.,
 Perez,Y.Y., Pham,T.L., Player,E.J., Primus,E.L., Pu,L., Puazo,M.,
 Purkiss,C., Qin,X., Quiroz,J.B., Rabata,D., Rachlin,E.K., Ren,Y.,
 Richards,S., Rojas,A., Ruiz,S., Sabo,A., Santibanez,J.,
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 Song,X., Sorelle,R.P., Svatek,A.F., Taylor,E.W., Taylor,T.R.,
 Thelus,R., Thomas,N., Thorn,R.D., Thornton,R.D., Tong,M.Y.,
 Trejos,Z.Y., Usmani,K., Vargo,C.E., Vattathil,S., Vega,R.A.,
 Villasana,D., Volkov,A., Walker,D.L., Wang,Q., Wang,S.,
 Warren,J.T., Watt,J.E., Wei,X., Wheeler,D.A., White,C.S., Williams
 jr,R.L., Williams,A.C., Williams,G.A., Williams,J.D., Wilson,K.,
 Woodworth,J.R., Worley,K.C., Wright,R.A., Wu,J., Wu,W., Yakub,S.,
 Yerrapragada,S., Yu,F., Yuan,D.T., Yuan,Y., Zhang,J., Zhang,L.,
 Zhang,Z., Zhou,J., Zhu,Y., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 195676)

AUTHORS Worley,K.C.

TITLE Direct Submission
 JOURNAL Submitted (16-FEB-2007) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 195676)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (14-APR-2007) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 COMMENT On Apr 14, 2007 this sequence version replaced gi:133754372.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help.tmc.edu
 ----- Project Information
 Center project name: LEYX
 Center clone name: CH250-65C9
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 200531 bases at least Q40
 Consensus quality: 200802 bases at least Q30
 Consensus quality: 200989 bases at least Q20
 Estimated insert size: 206589; sum-of-contigs estimation
 Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
 * The sequence data in this record represents an 'enhanced' version
 * of a Phase 2 submission. The indicated order and orientation of
 * each sequence has been established using one or more of the
 * following: read-pair data from individual subclones, overlaps
 * with neighboring clones, alignment with available reference
 * sequence (e.g., human), and/or confirmation by PCR testing.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 142140: contig of 142140 bp in length
 * 142141 142840: gap of 700 bp
 * 142841 154919: contig of 12079 bp in length
 * 154920 155019: gap of 100 bp

* 155020 160424: contig of 5405 bp in length
 * 160425 161324: gap of 900 bp
 * 161325 195676: contig of 34352 bp in length.

FEATURES Location/Qualifiers
 source 1. .195676
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 /mol_type="genomic DNA"
 /db_xref="taxon:9544"
 /clone="CH250-65C9"
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 /note="assembly_name:gap"
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 /estimated_length=700
 misc_feature 142841. .154919
 /note="assembly_name:Contig42"
 misc_feature 154920. .155019
 /note="assembly_name:gap"
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 /estimated_length=100
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 /note="assembly_name:Contig40"
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 /note="assembly_name:gap"
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 /estimated_length=900
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 /note="assembly_name:Contig59"

ORIGIN

Query Match 45.0%; Score 396.2; DB 16; Length 195676;
 Best Local Similarity 90.8%; Pred. No. 1.6e-107;
 Matches 433; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

Qy	333	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	392
Db	36045	AGTCTGGTTGGATGAGACAGGGTCGTGCCCCGATGATGGAGAACTCGACCCAGAAGCCTG	35986
Qy	393	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	452
Db	35985	AGGAGGTGTCGTGGATTTGTCTGGTGGGCTCCTGCTGCGGGTCCCAGCTTCAGGTGTCC	35926
Qy	453	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC	512
Db	35925	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTTGGATGGGAACTGAGCGAATCT	35866
Qy	513	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG	572
Db	35865	GGGTCTCCGCTGGGAGAGATGTGGCAGGACCAGCGAGGAATCCAGCCTGCCTGCTTCCGG	35806

Qy	573	AACAGTGT	TTTCCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	632
Db	35805	AACAGTGT	TTCCC-GACCCTGCTGAGTGGACTGGACCTCTGACACCTCCAGGGTCTTGCT	35747
Qy	633	GACTCCGGCCTGGT	GAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC	692
Db	35746	GACTCCAGCCTGGT	GCAAGGGAGCTCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC	35687
Qy	693	TCTCTTCTGGACA	AAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCCTGCC	752
Db	35686	TCTCTTCAGGACA	AAACACACCTTCCCAGCCCCACGGGCTGTGCAAATACGTGCCCCCTGCC	35627
Qy	753	ATAAGCACCAACA	AGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTT	809
Db	35626	ATAAGCACAAACA	AGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTTTTTTTTTTTTTT	35570

Search completed: April 28, 2009, 04:32:09
Job time : 937 secs

SCORE 3.0